

Claims

We claim:

5           1. A polynucleotide comprising:

          a) a nucleotide sequence encoding a mutant plant ethylene receptor protein, or a fragment thereof, wherein said mutant protein, or said fragment thereof, exhibits ethylene insensitivity; and

          b) a regulatory nucleotide sequence operably linked to said protein encoding nucleotide  
10       sequence, wherein said regulatory nucleotide sequence promotes transcription of said protein encoding nucleotide sequence in cells that comprise abscission zone tissue of a plant.

          2. The polynucleotide according to claim 1, wherein said mutant ethylene receptor protein is selected from the group consisting of *etr1*, *etr2*, *ers1*, *ers2*, and *ein4* mutant receptors.

15           3. The polynucleotide according to claim 2, wherein said *etr1* mutant receptor has a sequence of an *Arabidopsis thaliana* *etr1* sequence.

          4. The polynucleotide according to claim 3, wherein said *etr1* sequence is selected from  
20       the group consisting of *etr1*-1 (SEQ ID NO. 1), *etr1*-2 (SEQ ID NO. 2), *etr1*-3 (SEQ ID NO. 3), and *etr1*-4 (SEQ ID NO. 4).

          5. The polynucleotide according to claim 3, wherein said mutant receptor sequence is the *etr1*-1 sequence (SEQ ID NO. 1).

25           6. The polynucleotide according to claim 5, wherein said nucleotide sequence encoding said mutant receptor sequence comprises the sequence shown in SEQ ID NO. 5.

          7. The polynucleotide according to claim 2, wherein said *etr2* mutant receptor has a  
30       sequence of an *Arabidopsis thaliana* *etr2* sequence.

8. The polynucleotide according to claim 7, wherein the mutant receptor sequence is the *etr2-1* sequence (SEQ ID NO. 6).

9. The polynucleotide according to claim 8, wherein said nucleotide sequence encoding said mutant receptor sequence comprises the sequence shown in SEQ ID NO. 7.

10. The polynucleotide according to claim 1, wherein said regulatory nucleotide sequence comprises a promoter sequence from a plant chitinase gene, cellulase gene, or polygalacturonase gene.

11. The polynucleotide according to claim 10, wherein said promoter is from a cotton chitinase gene and comprises the nucleotide sequence shown in SEQ ID NO. 8 or a functional fragment thereof.

12. The polynucleotide according to claim 1, wherein said protein encoding nucleotide sequence encodes a mutant receptor sequence having the amino acid sequence shown in SEQ ID NO. 1, and wherein said regulatory nucleotide sequence comprises the sequence shown in SEQ ID NO. 8 or a functional fragment thereof.

13. The polynucleotide according to claim 10, wherein said promoter is from a cotton chitinase gene.

14. A cell transformed with a polynucleotide that comprises:

a) a nucleotide sequence encoding a mutant plant ethylene receptor protein, or a fragment thereof, wherein said mutant protein, or said fragment thereof, exhibits ethylene insensitivity; and

b) a regulatory nucleotide sequence operably linked to said protein encoding nucleotide sequence, wherein said regulatory nucleotide sequence promotes transcription of said protein encoding nucleotide sequence in cells that comprise abscission zone tissue of a plant.

15. A plant, plant tissue, or a plant cell transformed with or bred to contain a polynucleotide that comprises:

a) a nucleotide sequence encoding a mutant plant ethylene receptor protein, or a fragment thereof, wherein said mutant protein, or said fragment thereof, exhibits ethylene insensitivity; and

b) a regulatory nucleotide sequence operably linked to said protein encoding nucleotide sequence, wherein said regulatory nucleotide sequence promotes transcription of said protein encoding nucleotide sequence in cells that comprise abscission zone tissue of a plant.

16. The plant, plant tissue, or a plant cell according to claim 15, wherein said mutant ethylene receptor protein is selected from the group consisting of etr1, etr2, ers1, ers2, and ein4 mutant receptors.

17. The plant, plant tissue, or a plant cell according to claim 15, wherein said etr1 mutant receptor has a sequence of an *Arabidopsis thaliana* etr1 sequence.

18. The plant, plant tissue, or a plant cell according to claim 17, wherein said etr1 sequence is selected from the group consisting of etr1-1 (SEQ ID NO. 1), etr1-2 (SEQ ID NO. 2), etr1-3 (SEQ ID NO. 3), and etr1-4 (SEQ ID NO. 4).

19. The plant, plant tissue, or a plant cell according to claim 18, wherein the mutant receptor sequence is the etr1-1 sequence (SEQ ID NO. 1).

20. The plant, plant tissue, or a plant cell according to claim 19, wherein said nucleotide sequence encoding said mutant receptor sequence comprises the sequence shown in SEQ ID NO. 5.

21. The plant, plant tissue, or a plant cell according to claim 16, wherein said etr2 mutant receptor has a sequence of an *Arabidopsis thaliana* etr2 sequence.

22. The plant, plant tissue, or a plant cell according to claim 21, wherein the mutant receptor sequence is the *etr2-1* sequence (SEQ ID NO. 6).

23. The plant, plant tissue, or a plant cell according to claim 22, wherein said nucleotide sequence encoding said mutant receptor sequence comprises the sequence shown in SEQ ID NO. 7.

24. The plant, plant tissue, or a plant cell according to claim 15, wherein said regulatory nucleotide sequence comprises a promoter sequence from a plant chitinase gene, cellulase gene, or polygalacturonase gene.

25. The plant, plant tissue, or a plant cell according to claim 24, wherein said promoter is from a cotton chitinase gene and comprises the nucleotide sequence shown in SEQ ID NO. 8 or a functional fragment thereof.

26. The plant, plant tissue, or a plant cell according to claim 15, wherein said protein encoding nucleotide sequence encodes a mutant receptor sequence having the amino acid sequence shown in SEQ ID NO. 1, and wherein said regulatory nucleotide sequence comprises the sequence shown in SEQ ID NO. 8 or a functional fragment thereof.

27. The plant, plant tissue, or a plant cell according to claim 15, wherein said plant is a monocotyledonous plant.

28. The plant, plant tissue, or a plant cell according to claim 27, wherein said monocotyledonous plant is selected from the group consisting of rice, wheat, barley, oats, rye, sorghum, maize, lilies, banana, pineapple, turfgrass, gladiolus, and millet.

29. The plant, plant tissue, or a plant cell according to claim 15, wherein said plant is a dicotyledonous plant.

30. The plant, plant tissue, or a plant cell according to claim 29, wherein said dicotyledonous plant is selected from the group consisting of cotton, peas, alfalfa, chickpea, chicory, clover, kale, lentil, prairie grass, soybean, tobacco, potato, sweet potato, radish, cabbage, rape, apple trees, coffee, tomato, melon, citrus, beans, roses, sugar beet, squash, peppers, strawberry, carnation, chrysanthemums, impatiens, eucalyptus, and lettuce.

31. A method for decreasing flower, fruit, or leaf drop in a plant upon exposure to ethylene, said method comprising introducing a polynucleotide into said plant, wherein said polynucleotide comprises:

a) a nucleotide sequence encoding a mutant plant ethylene receptor protein, or a fragment thereof, wherein said mutant protein, or said fragment thereof, exhibits ethylene insensitivity; and

b) a regulatory nucleotide sequence operably linked to said protein encoding nucleotide sequence, wherein said regulatory nucleotide sequence promotes transcription of said protein encoding nucleotide sequence in cells that comprise abscission zone tissue of a plant.

32. The method according to claim 31, wherein said mutant ethylene receptor protein is selected from the group consisting of *etr1*, *etr2*, *ers1*, *ers2*, and *ein4* mutant receptors.

33. The method according to claim 32, wherein said *etr1* mutant receptor has a sequence of an *Arabidopsis thaliana* *etr1* sequence.

34. The method according to claim 33, wherein said *etr1* sequence is selected from the group consisting of *etr1*-1 (SEQ ID NO. 1), *etr1*-2 (SEQ ID NO. 2), *etr1*-3 (SEQ ID NO. 3), and *etr1*-4 (SEQ ID NO. 4).

35. The method according to claim 34, wherein the mutant receptor sequence is the *etr1*-1 sequence (SEQ ID NO. 1).

36. The method according to claim 35, wherein said nucleotide sequence encoding said mutant receptor sequence comprises the sequence shown in SEQ ID NO. 5.

37. The method according to claim 32, wherein said *etr2* mutant receptor has a sequence  
5 of an *Arabidopsis thaliana* *etr2* sequence.

38. The method according to claim 37, wherein the mutant receptor sequence is the *etr2*-1 sequence (SEQ ID NO. 6).

10 39. The method according to claim 38, wherein said nucleotide sequence encoding said mutant receptor sequence comprises the sequence shown in SEQ ID NO. 7.

40. The method according to claim 31, wherein said regulatory nucleotide sequence comprises a promoter sequence from a plant chitinase gene, cellulase gene, or polygalacturonase  
15 gene.

41. The method according to claim 40, wherein said promoter is from a cotton chitinase gene and comprises the nucleotide sequence shown in SEQ ID NO. 8 or a functional fragment thereof.  
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42. The method according to claim 31, wherein said protein encoding nucleotide sequence encodes a mutant receptor sequence having the amino acid sequence shown in SEQ ID NO. 1, and wherein said regulatory nucleotide sequence comprises the sequence shown in SEQ ID NO. 8 or a functional fragment thereof.  
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43. The method according to claim 31, wherein said plant is a monocotyledonous plant.

44. The method according to claim 43, wherein said monocotyledonous plant is selected from the group consisting of rice, wheat, barley, oats, rye, sorghum, maize, lilies, banana,  
30 pineapple, turfgrass, gladiolus, and millet.

45. The method according to claim 31, wherein said plant is a dicotyledonous plant.

46. The method according to claim 45, wherein said dicotyledonous plant is selected from the group consisting of cotton, peas, alfalfa, chickpea, chicory, clover, kale, lentil, prairie grass, soybean, tobacco, potato, sweet potato, radish, cabbage, rape, apple trees, coffee, tomato, melon, citrus, beans, roses, sugar beet, squash, peppers, strawberry, carnation, chrysanthemums, impatiens, eucalyptus, and lettuce.

47. A polynucleotide comprising:

a) a nucleotide sequence encoding a plant *EIN* or *EIL* gene product, or a fragment thereof; and

b) a regulatory nucleotide sequence operably linked to said protein encoding nucleotide sequence, wherein said regulatory nucleotide sequence promotes transcription of said protein encoding nucleotide sequence in cells that comprise abscission zone tissue of a plant.

48. The polynucleotide according to claim 47, wherein said *EIN* gene product is an *EIN2* or *EIN3* gene product.

49. The polynucleotide according to claim 47, wherein said *EIL* gene product is an *EIN3-like* gene product.

50. The polynucleotide according to claim 47, wherein said regulatory nucleotide sequence comprises a promoter sequence from a plant chitinase gene, cellulase gene, or polygalacturonase gene.

51. The polynucleotide according to claim 50, wherein said promoter is from a cotton chitinase gene and comprises the nucleotide sequence shown in SEQ ID NO. 8 or a functional fragment thereof.

52. A polynucleotide comprising:

a) a nucleotide sequence whose transcribed nucleic acid sequence is at least partially complementary to the transcription product of an *EIN* or *EIL* gene, or a fragment thereof; and

b) a regulatory nucleotide sequence operably linked to said protein encoding nucleotide sequence, wherein said regulatory nucleotide sequence promotes transcription of said protein encoding nucleotide sequence in cells that comprise abscission zone tissue of a plant.

53. The polynucleotide according to claim 52, wherein said *EIN* gene is an *EIN2* or *EIN3* gene.

54. The polynucleotide according to claim 52, wherein said *EIL* gene is an *EIN3-like* gene.

55. The polynucleotide according to claim 52, wherein said regulatory nucleotide sequence comprises a promoter sequence from a plant chitinase gene, cellulase gene, or polygalacturonase gene.

56. The polynucleotide according to claim 55, wherein said promoter is from a cotton chitinase gene and comprises the nucleotide sequence shown in SEQ ID NO. 8 or a functional fragment thereof.